Improvement of sweet sorghum for drought tolerance

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SSEA 2014 Annual Meeting, 23 Jan Orlando

International Crops Research Institute for the Semi-Arid Tropics

Vision

A prosperous, food-secure and resilient dryland tropics

Mission

To reduce poverty, hunger, malnutrition and environmental degradation in the dryland tropics

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IMOD: A new approach

Inclusive Market-Oriented Development (IMOD)

Outline of presentation

- Introduction to ICRISAT
- Why sweet sorghum?
- Biopower strategy
- Genetic resources
- Screening for drought
- Breeding efforts and methodology
- MABS
- Conclusions

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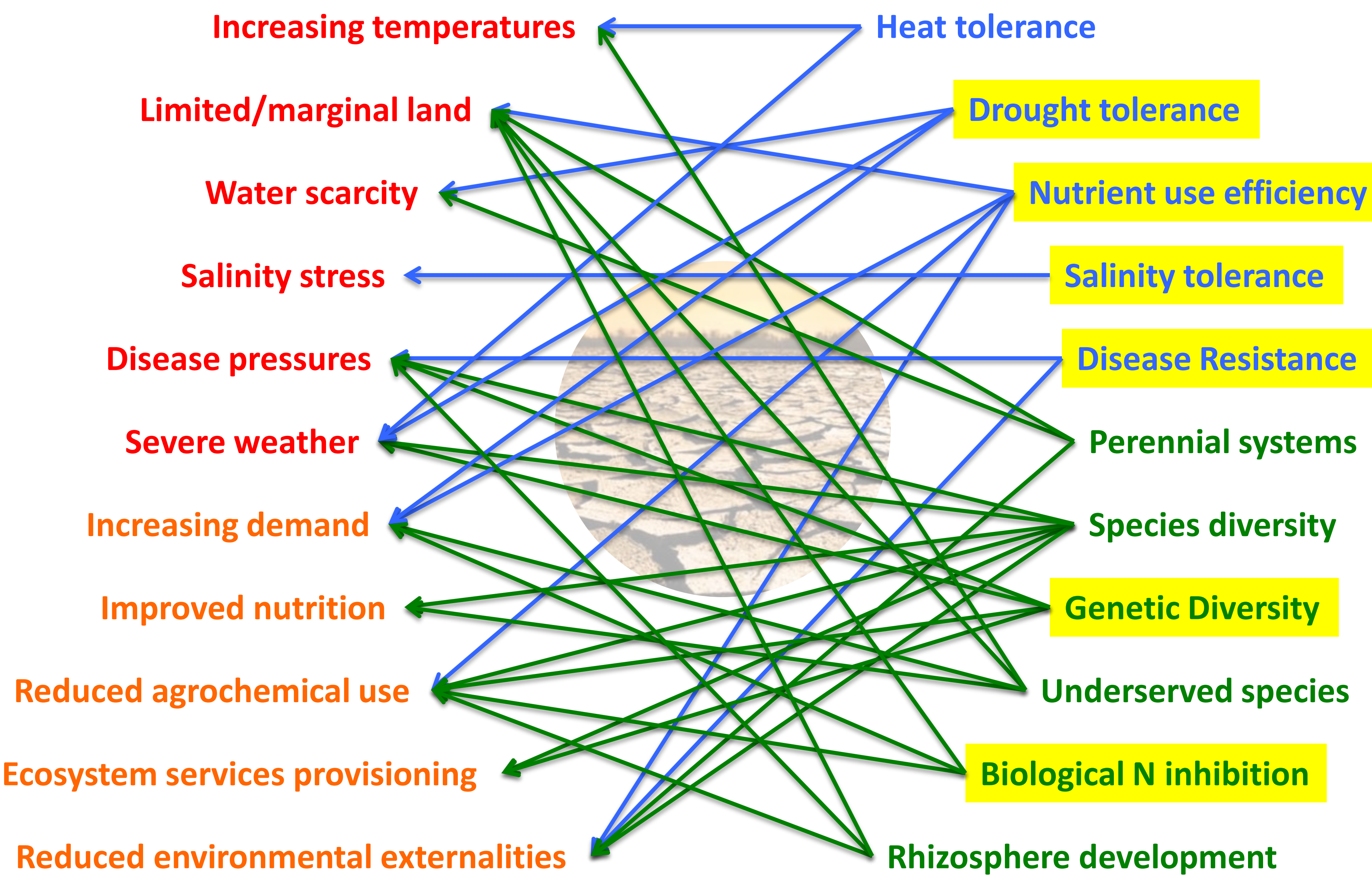
Breeding crops for the future



ICRISAT's BioPower strategy

- BioPower empowers the dryland poor to benefit from emerging bioenergy opportunities
- Ensures both food and energy security
- Focuses on biomass, juice and grain yields
- Greater smallholder incomes
- Sustaining environments




Tradeoff between food and fuel

Season	Variety/ hybrid	Sugar yield (t ha^{-1})			Grain yield (t ha^{-1})		
		Sweet stalks (SS)	Non-sweet stalks	% gain of SS	Sweet stalks (SS)	Non-sweet stalks	% gain / loss in SS
Rainy season	Varieties	6.0 (6)[1]	3.9 (11)	54	3.0 (6)	3.3 (11)	-9
	Hybrids	6.2 (5)	5.6 (4)	11	6.2 (5)	5.9 (4)	5
Post rainy season	Varieties	1.7 (11)	0.9 (6)	89	4.6 (11)	4.7 (6)	-2
	Hybrids	1.5 (6)	1.0 (3)	50	6.4 (6)	8.5 (3)	-25

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Sorghum R-lines

Type	Number of entries
A_1- Early	220
A_1-Medium	359
A_1-Late	70
Total	649
A_2- Medium	145
A_1 and A_2	82
A_3	13
A_4	13
A_1, A_2 and A_3	2
Total	255

Sweet sorghum – energy (ethanol)

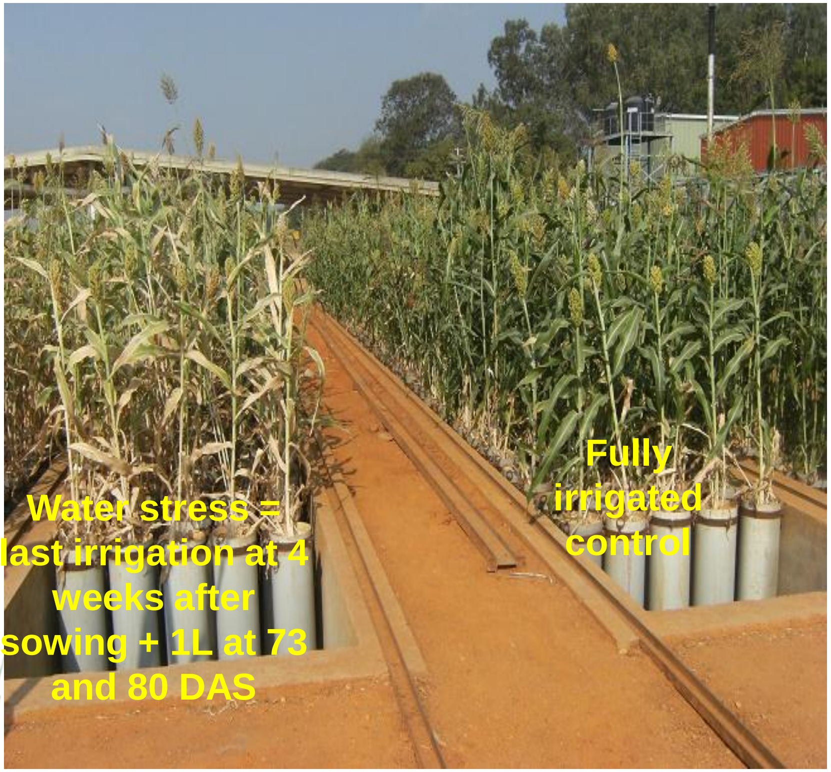
ICSA 38 x SSV 84 (CSH 22SS)

Source of sorghum germplasm resistant/adapted for drought in rabi seasons (Source: ICRISAT/NRCS)

Drought	Sources/IS lines	R lines/Varieties	Parental lines
Seedling emergence	IS 301, Naga white, D 71463, D 71464	IS 2877, IS 1045*, D 38061, D 38093, D 38060, ICSV 88050, 88065, SPV 354	VZM1-B, 2077B
Early	ISs 824, 1037*, 3477, 6928, 8370, 10596, 10701, 12611, E 36-1, DJ 1195*	ICSVs 88056, 88057, 88059, 88063, IS 24025, SAR 35, DKVs 3, 4, 17, 18	ICSBs 3, 6, 11, 37, 54, 88001, 2219B
Mid-season	ISs 1347, 13441, DJ 1195*	ICSVs 213, 221, 210, 272, 273, 295, 378, 572, Ds 71463, 71464, DKVs 1, 3, 7	ICSBs 58, 196B, 2077B
Terminal	DJ 1195*, M 35-1*, IS 22314, IS 22380, E 185-2, IS 12611, IS 6928	D 38001, D 71283, D 71464, IS 13441, DKVs 3, 4, 17, 18	ICSB 17, 296B

Lysimetric studies

Assessment of 152 sorghum accessions from the reference collection for terminal drought stress in lysimeters



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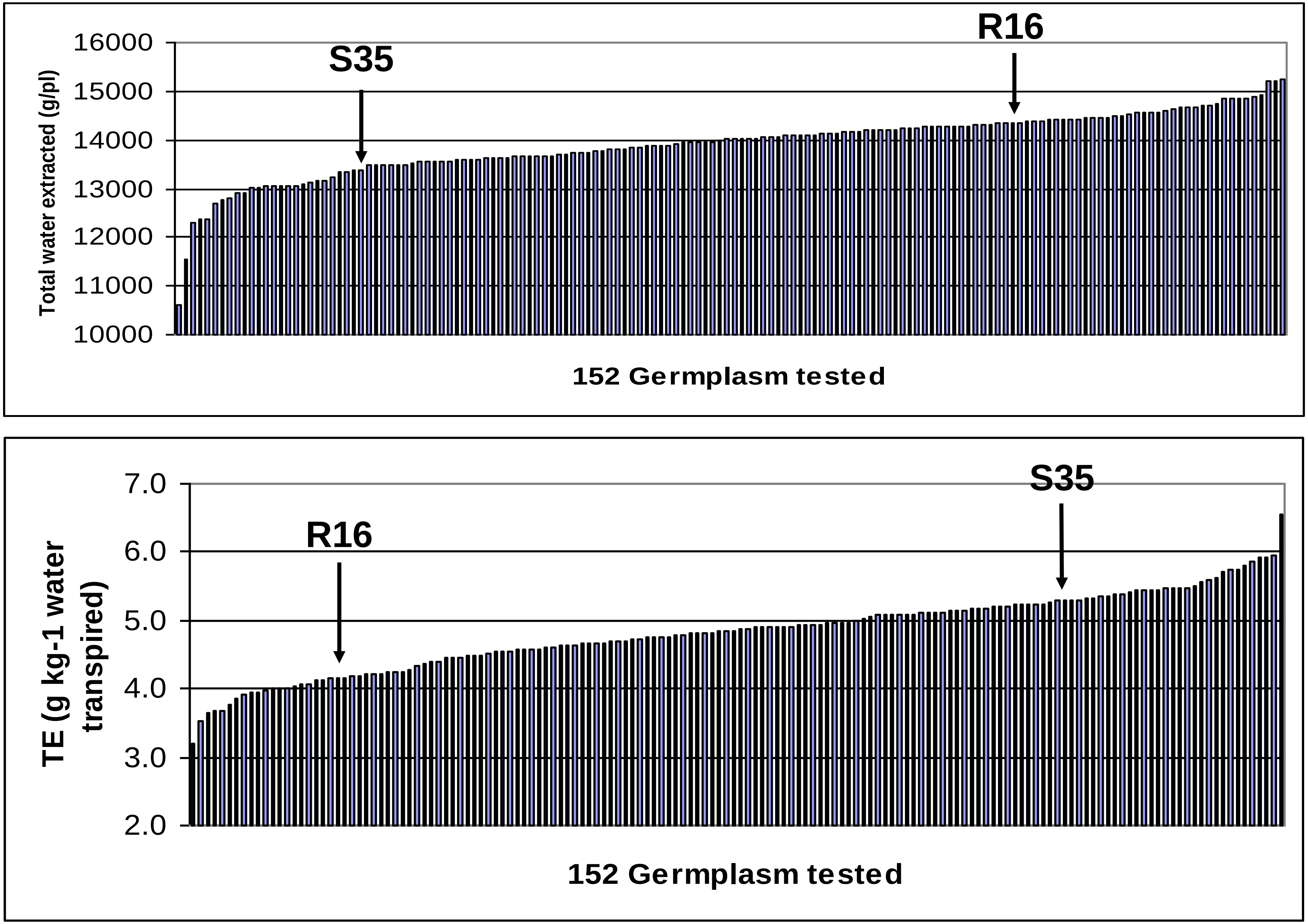
Large variation in water extraction and TE differences under WS



Vadez et al., 2011 Crop & Pasture Scienc

Selection scheme for drought

Sweet Fuel

New material added

Screening for midseason stress 2009

393: 100 B lines, 170 R lines, 68 F_1s and 58 GA

Screening for midseason stress 2010 (240 Genotypes)

Evaluation for SAT rainy adaptation 2009

95: 56 B lines, 5 R lines, 27 F_1s and 1GA

240: 5 B lines, 88 R lines, 80 F_1s, 39 F_6s and 3GA

Screening for terminal stress 2009

Evaluation for SAT post rainy adaptation 2009

95: 56 B lines, 5 R lines, 27 F_1s and 1GA

Screening for midseason stress 2011 (95 Genotypes)

Evaluation for SAT rainy adaptation 2011 (68 Genotypes)

Evaluation for SAT post rainy adaptation 2010 (42 Genotypes)

Screening for terminal stress 2011 (17 sweet sorghum varieties)

Evaluation for SAT post rainy adaptation 2010 (42 Genotypes)

New material added

280: 135 B lines, 100 R lines, 45 HBM lines

Screening for midseason stress 2012 (280 Genotypes)

Evaluation for SAT rainy adaptation 2012 (24 Genotypes)

384: 185 B lines, 129 R lines, 66 HBM lines

Screening for midseason stress 2013 (280 Genotypes)

Screening for terminal stress 2013 (77 sweet sorghum lines)

Evaluation for SAT rainy adaptation 2013 (25 Genotypes)

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Screening for terminal stress

Susceptible genotypes under terminal stress

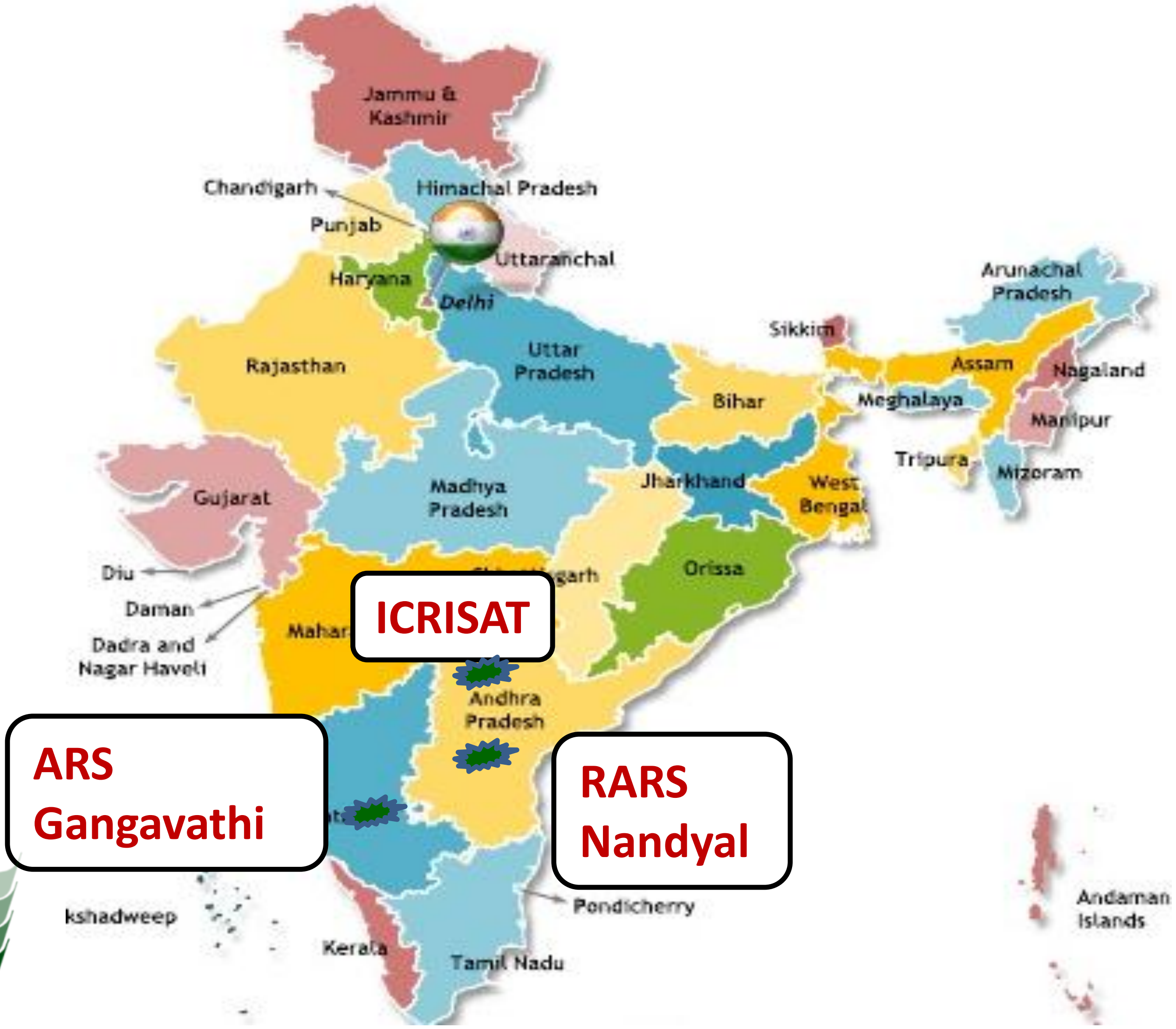
Tolerant genotypes under terminal stress

Screening for midseason stress

Productive genotypes under drought

Genotypes showing varied drought tolerance mechanisms

MLTs for terminal stress screening



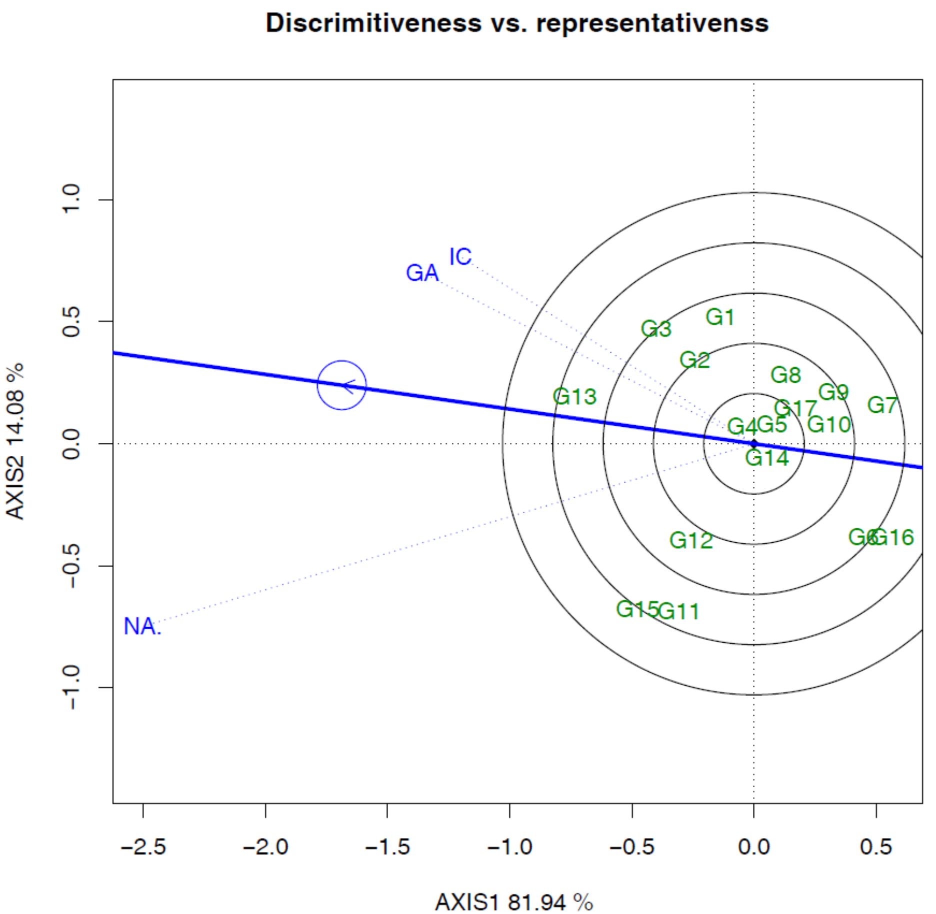
Sorghum hybrid female parents

ICSA numbers			Traits	No. of lines
1 to 103			High yielding	77
88001 to 88026			"	15
89001 to 89004			"	4
90001 to 90004			"	4
91001 to 91010			"	10
94001 to 94012			"	12
201 to 259			Downy mildew resistant	59
260 to 295			Anthracnose resistant	36
296 to 328			Leaf blight resistant	33
329 to 350			Rust resistant	22
351 to 408			Grain mold resistant	58
409 to 436			Shoot fly resistant (rainy)	28
437 to 463			Shoot fly resistant (postrainy)	27
464 to 474			Stem borer resistant (rainy)	11
475 to 487			Stem borer resistant (postrainy)	13
488 to 545			Midge resistant	58
546 to 565			Head bug resistant	20
566 to 599			Striga resistant	34
600 to 614			Acid soil tolerant lines	15
615 to 637			Early-maturity lines	23
638 to 670			Durra (large grain) lines	33
671 to 687			Tillering and stay green lines	17
688 to 738			Non-milo (A_2) cytoplasmic lines	51
739 to 755			Non-milo (A_3) cytoplasmic lines	17
756 to 767			Non-milo (A_4) cytoplasmic lines	12
29001 to 29005 & 29017			Shoot fly resistant (rainy)	6
29006 to 29016			Grain mold resistant	16
Total				711

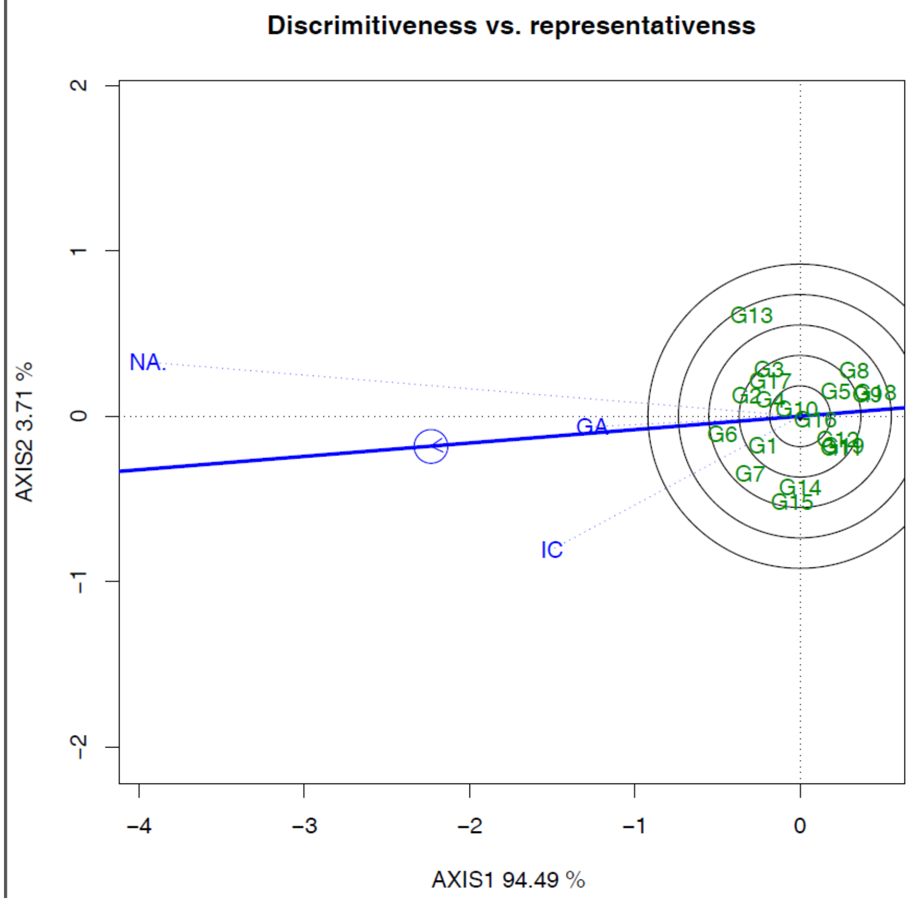
Analysis of Variance

Source of variation	d.f.	Days to 50 % flowering	Plant height (m)	Stalk weight (t ha^{-1})	Juice weight (t ha^{-1})	Brix (%)	Sugar yield (t ha^{-1})	Grain Yield (t ha^{-1})
Location	2	**2031.9****	**1.37****	**6690 ****	**1057 ****	**435.54****	**5.29****	**37.62****
Residual	6	0.57	0.02	11.53	1.37	1.27	0.01	1.3
Genotype	16	**61.43****	**2.16****	**885.69****	**143.44****	**35.42****	**1.62****	**4.56****
Genotype x Location	32	**16.75****	**0.06****	**203.09****	**28.56****	**4.58****	**0.26****	**1.28**

GGE Biplot in Terminal and Mid-season stress

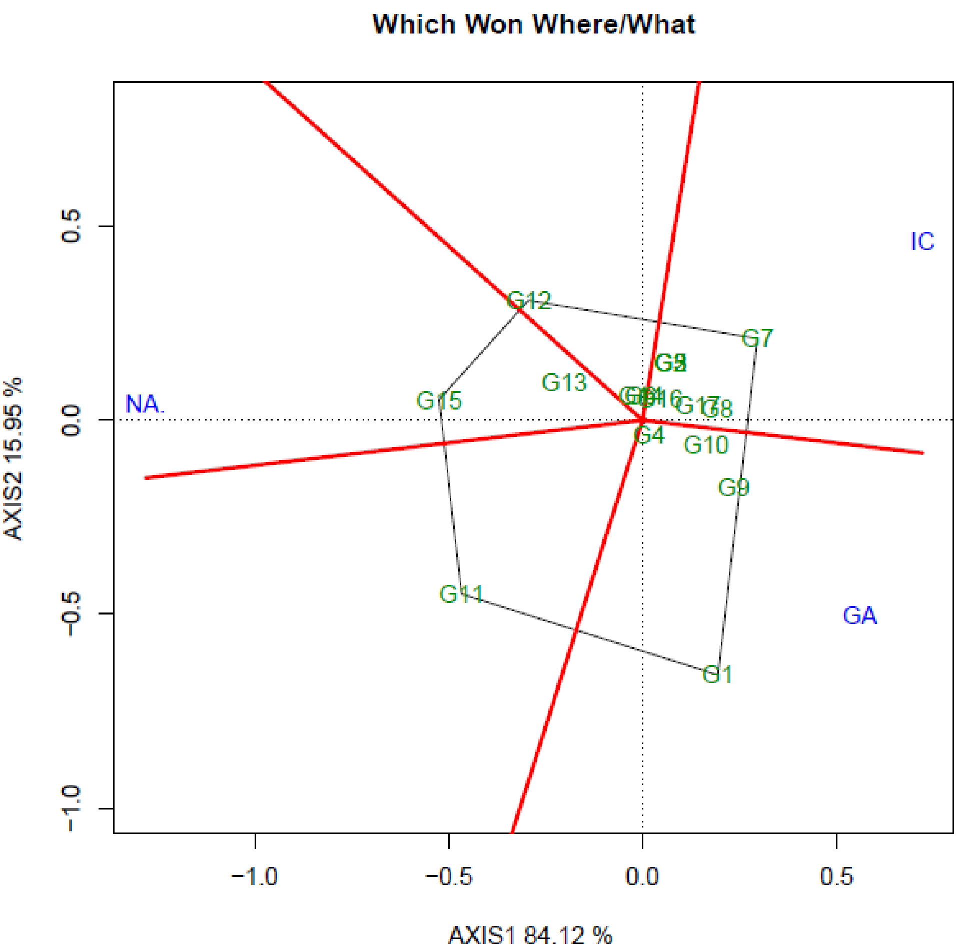


Terminal stress

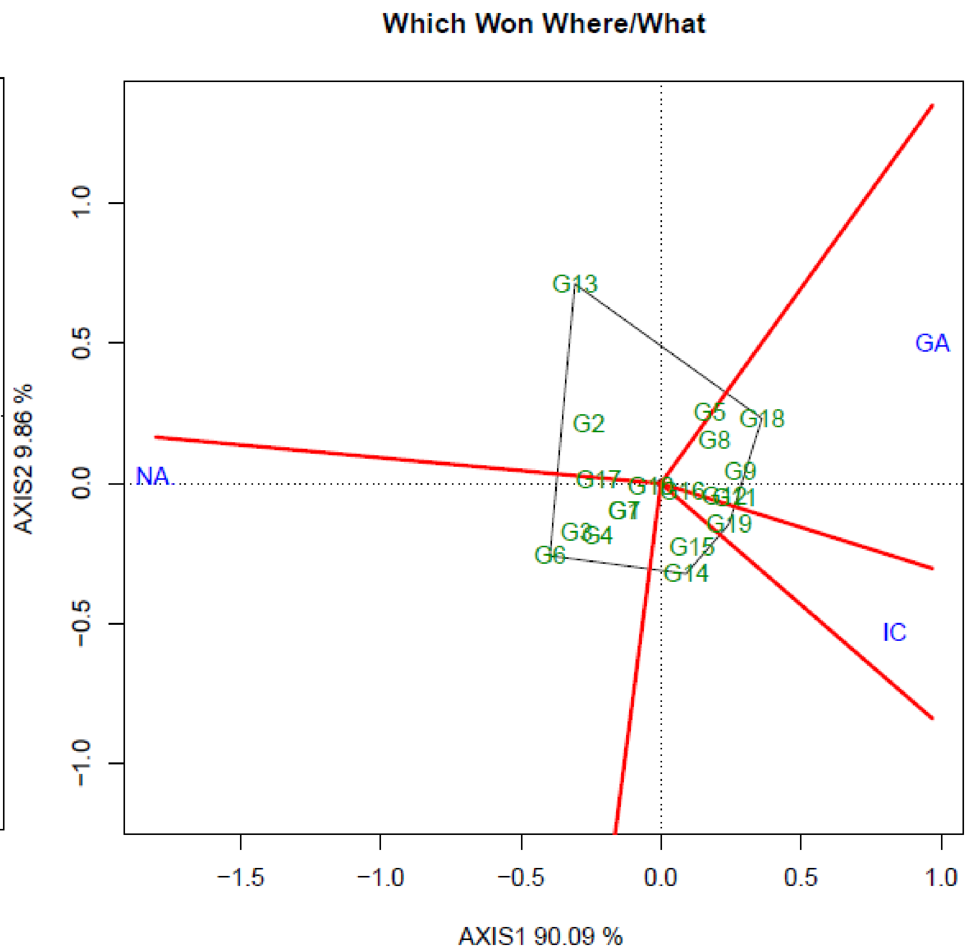


Mid-season stress

GGE Biplot on Which won where in Terminal and Mid-season stress



Terminal stress



Mid-season stress

Conclusions

- Nandhyal is most distinguishing environment for drought screening
- ICRISAT Patancheru: OPV 17, ICSSH 47 and ICSV 25311
- RARS Nandyal: ICSV 93046, OPV 17 and OPV 3
- ARS Gangavathi: ICSV 25311 and ICSSH 47

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Midseason and terminal drought stress studies at ICRISAT

Glasshouse studies

Lysimetric studies

Field studies

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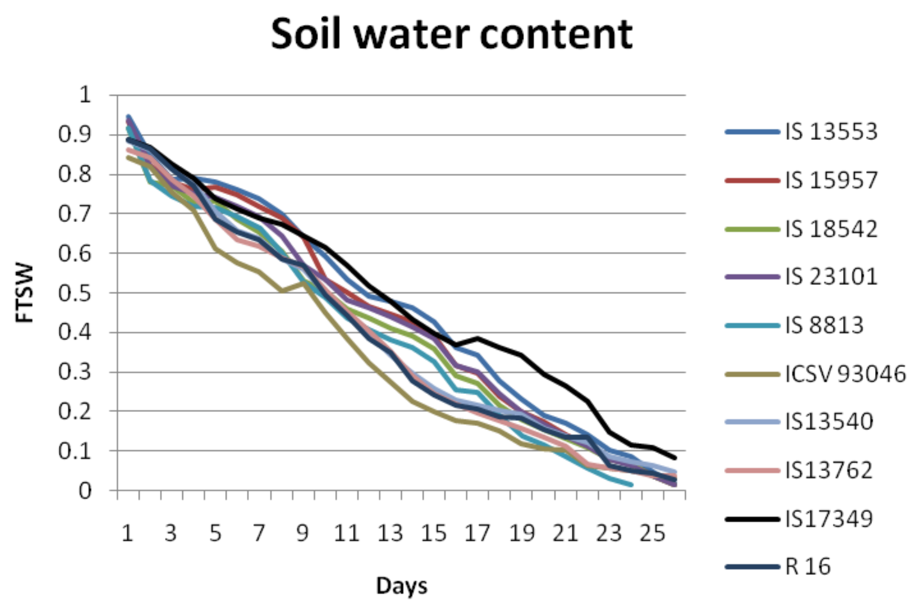
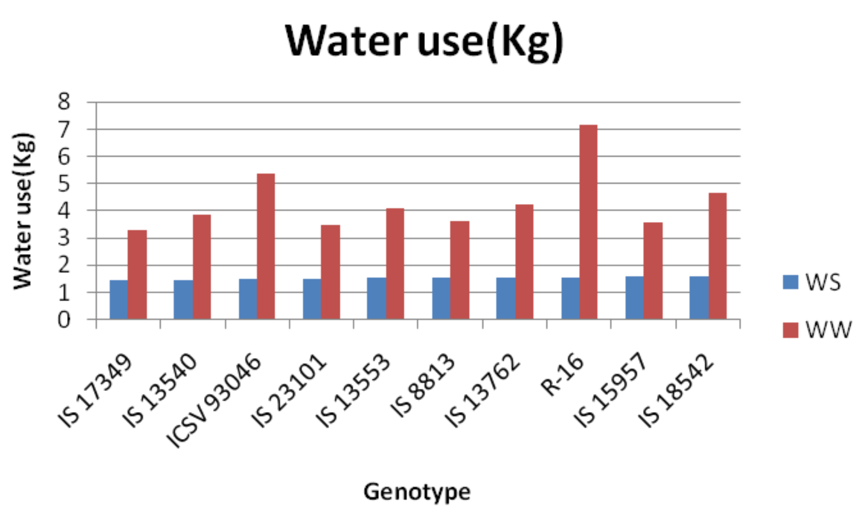
Evaluation of high biomass lines for mid season drought tolerance & water use efficiency in glasshouse



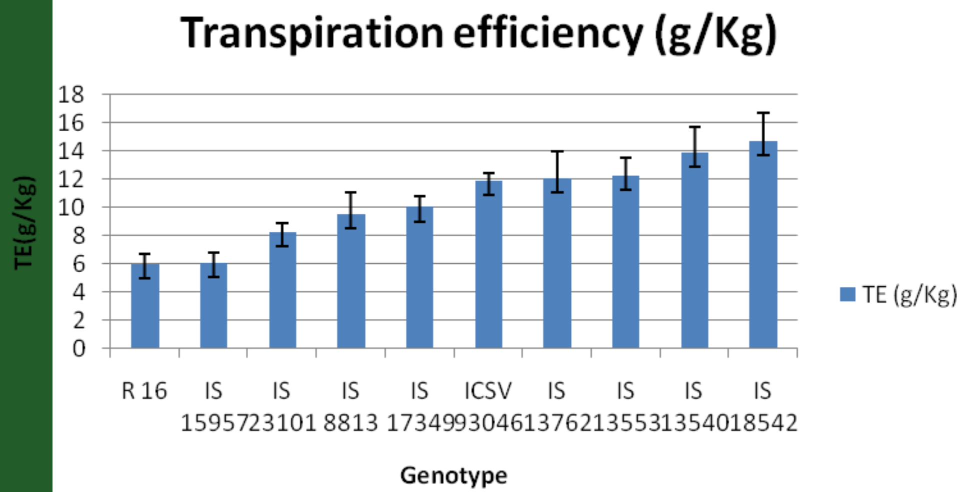


FTSW: Fraction of transpirable soil water

- ✓ Dynamics of water Extraction differed
- ✓ Some genotypes showed slower water use which in turn led to longer maintenance of soil moisture

TE & Water use

TE: grams of biomass accumulated per 1Kg of water transpired



Genotype	Transpiration efficiency (TE)(g)	Water use(kg)
	WW	WW
IS 13540	13.84	3.848
IS 13762	12.02	4.240
IS 17349	10.00	3.273
ICSV 93046	11.86	6.662
R 16	5.96	7.168
IS 13553	13.88	4.09
IS 15957	6.83	3.58
IS 18542	16.64	4.65
IS 23101	9.29	3.5
IS 8813	10.8	3.63

✓There were significant differences in TE
✓Low TE genotype (R-16) is highly senescent post rainy cultivar

Transpiration efficiency is high for IS 13540,IS 13553and IS 18542 compared with checks R-16 and ICSV 93046

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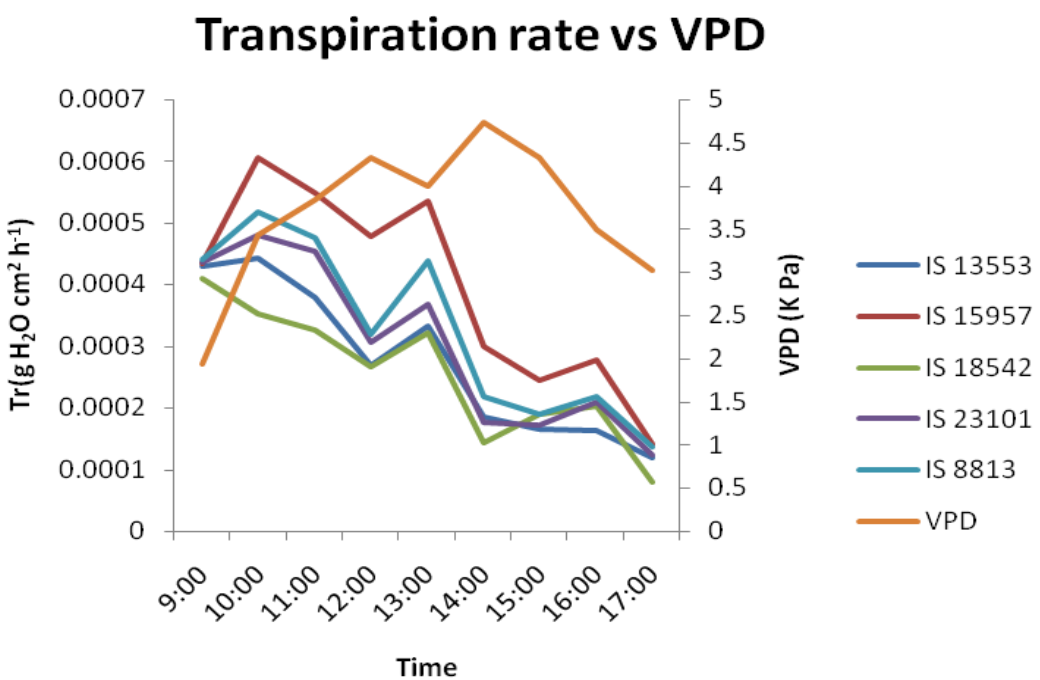
Vapour Pressure Deficit (VPD) response



Transpiration rates of selected genotypes under different VPD conditions

- **Well watered conditions defines the water stress conditions.**
- **Well watered transpiration rate (Tr) of tolerant genotype was lower than sensitive genotypes at all VPD levels.**

Sweet sorghum varieties tested for terminal drought stress in lysimeters (Summer 2013)

Genotype	Wat Extracted (ml)	Days to boot	Days to flower	Tot Stover DW (t/ha)	Tot Panicle DW (t/ha)	Tot Grain DW (t/ha)	Tot DW t/ha)	TE (g/Kg)
ICSV 25299	9500	59.6	63.8	60.4	38.0	26.8	98.4	5.07
ICSV 25300	7784	56.75	61.25	46.7	41.8	32.9	88.5	4.05
ICSV 25303	8668	61.8	66.6	58.5	39.2	23.0	97.7	4.94
ICSV 25307	8588	58	63.4	62.8	26.9	18.9	89.8	4.25
ICSV 25308	9220	57	61.4	73.5	36.4	25.0	109.9	4.78
ICSV 25311	8860	56.6	61.2	60.0	36.3	27.5	96.2	4.92
ICSV 25315	10088	60.6	65.6	74.1	40.9	30.6	114.9	5.40
ICSV 25316	8464	59	63.25	61.7	35.3	27.8	97.0	4.19
ICSV 25333	11608	65.25	70.25	89.0	15.7	6.1	104.7	4.84
ICSV 25334	10060	60.6	66.4	69.4	30.1	19.1	99.5	4.77
ICSV 25340	7780	58.4	63	42.3	43.1	34.4	85.5	5.40
ICSV 25341	9864	56.8	61.8	63.7	63.1	53.2	126.8	5.45
IS 18542	8164			81.3	0.8	0.8	82.1	3.84
ICSV 93046	10192	61.8	66.4	72.2	30.4	21.3	102.6	4.79
E 36-1	5840	55.2	59.8	44.4	33.9	27.4	78.3	4.91
CV%	29	4.9	4.9	41.3	49	13.4	35.2	25.6
LSD (5% level)	3293.3	3.6	3.9	33.5	21.19	18.17	43.74	1.54

Mid-season stress trial, 2013

- ✓ 189 B lines with checks viz., B 35, ICSV 93046, R 16, ICSV 25316 (SP 2061-2), ICSB 38, E 36
- ✓ The top five entries for highest stalk yield : SP 08 2036-2, ICSB 307, SP 54819-1, ICSB 73 and ICSB 11023 (ICSB 38: 16 t ha^{-1})
- ✓ 129 R lines with checks *viz.,* NTJ-2, E 36-1, ICSV 25316, ICSV 93046, B 35, R 16 and ICSV 112 .
- ✓ The top five entries for sugar yield include (Ch-11 x E 36-1)-10-1-1, ICSV 12022, (Ch-1 x (DSV 4 x SSV 84)-1-2-1-1)-13-3-3-3, (Ch-1 x (ICSV 93046 x SSV 84)-7-2-1-1)-4-1-1-7 and ICSV 12016 (Urja: 1.3 t ha^{-1})
- ✓ 66 high biomass lines including the checks viz., CSH 22 SS and ICSV 93046
- ✓ The top 5 entries for higher fresh stalk yield include IS 25340, IS 18542, IS 21893, IS 13553 and IS 3062 (ICSV 93046: 29.5 t ha^{-1})

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MAB breeding for major stay-green QTLs

- **Sources: <u>B 35</u>, <u>E 36-1</u>, <u>SC 56</u> and KS 19**
- **At ICRISAT, thru MAB- QTLs introgressed in to two genetic backgrounds (*viz*., R16 and S35) accomplished**
- **The resulting products (BC_3F_5s and BC_4F_4s) evaluated both in multi-location trials as well as in lysimetry/tube experiments, and the most stay green ones identified**

Expression of stay-green trait in sorghum from E 36-1

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Introgression of Stay Green QTLs into Sweet sorghum lines

Objective : To tackle the post flowering drought stress through introgression of Stay green QTLs into elite sweet sorghum varieties and hybrid parents

Season : Post Rainy-2013

Generation : BC_2F_1's (3) and BC_3F_1's (4)

Donor parents : 19-35-SG-06019 (stg3) and
19-35-SG-06002 (stgA)

Recurrent parent : Sweet sorghum lines

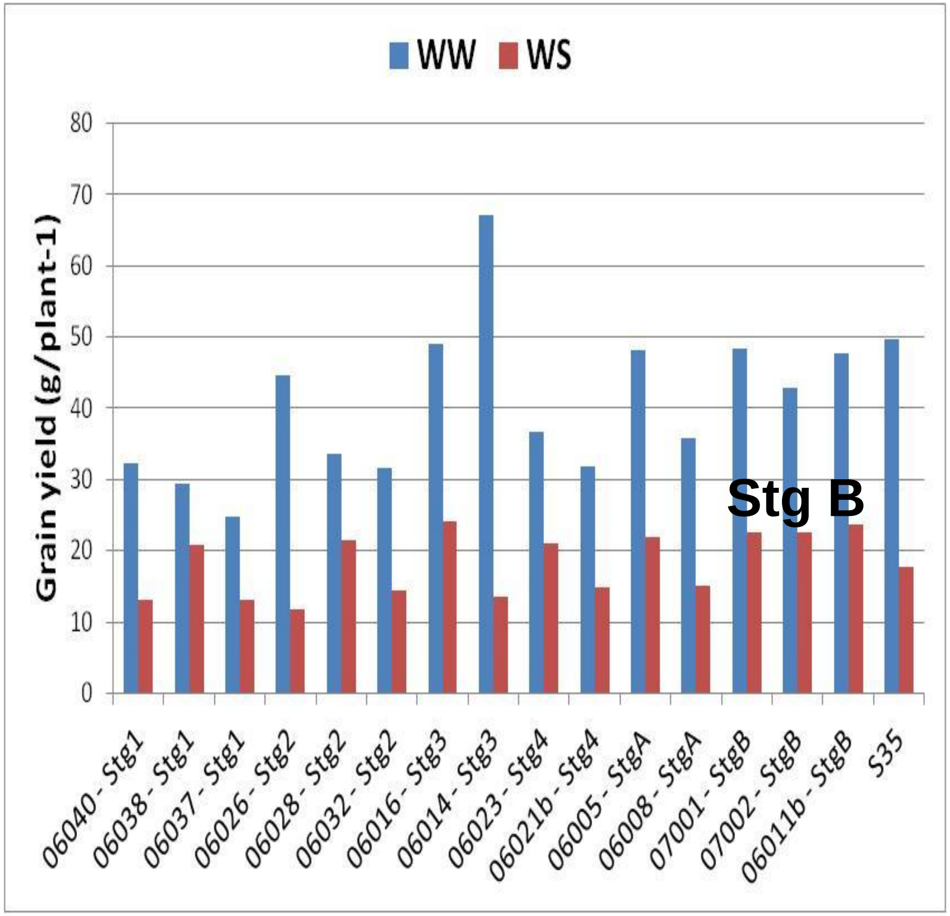
BC population : BC_3F_1's (4)

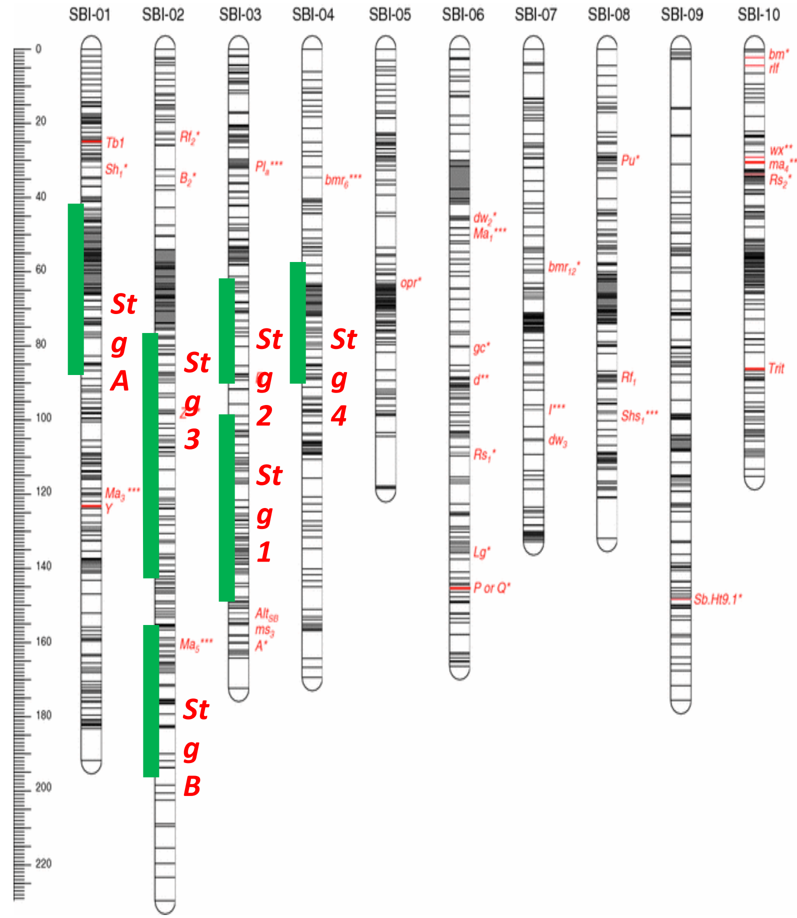
19-35-SG-06019 x ICSB 479 (1)
19-35-SG-06019 x SP 35769 (1)
19-35-SG-06019 x SP 35878 (2)

: BC_2F_1's (3)

19-35-SG-06002 x ICSV 25308 (2)
19-35-SG-06002 x IS 23789 (1)

StgB QTL introgressed in to S 35 background





Source: Mace et al., 2010

SSR Markers for Foreground Selection

SSR locus	B35 Stay-green QTL	Putative marker order	Physical genomic distance	Forward-primer sequence	Reverse-primer sequence	Reference
Xtxp013	stg3	1	55.9500	TCTTTCCCAAGGAGCCTAG	GAAGTTATGCCAGACATGCTG	Kong et al. 2000
Xtxp298	stgB	2	57.0810	GCATGTGTCAGATGATCTGGTGA	GCTGTTAGCTTCTTCTAATCGTCGGT	Bhattramakki et al. 2000
XSbAGB03	stg3	3	58.1280	AGCTCTCAGCCTTTCCACAAT	GGAAGAAAGGAATGACTTGA	Taramino et al. 1997
Xcup63	stg3	4	59.1046	GTAAAGGGCAAGGCAACAAG	GCCCTACAAAATCTGCAAGC	Schloss et al. 2002
Xtxp445	stg3	5	60.4532	GCCAGTTGAATCCGCTACAT	GAATTGCAATACATAAGCACACC	
Xcup29	stg3	6	60.4534	CTTTCTCGATTTCTGGTGCC	TTTACCTTGCCTATGCCTGC	Schloss et al. 2002
Xtxp430	stg3	7	61.0898	AGTATTTGCCGCTGGTGAAG	TCTCGATTTCGACAGGCTTT	
Xtxp001	stg3	8	61.3678	TTGGCTTTTGTGGAGCTG	ACCCAGCAGCACTACACTAC	Kong et al. 2000
Xtxp056	stg3	9	61.5686	TGTCTTCGTAGTTGCGTGTTG	CCGAAGGAGTGCTTTGGAC	Bhattramakki et al. 2000
Xisep0938	stg3	10	63.4368	TGCTGTTCTTGAACGTGTTTG	TTTTGCACAAAGTTGCGTGT	Ramu et al. 2009
Xgap84	stg3	11		CGCTCTCGGGATGAATGA	TAACGGACCACTAACAAATGATT	Brown et al. 1996
Xtxp019	stg3	12		CTTTCAATCGGTTCCAGAC	CTTCCACCTCCGTACTC	Kong et al. 2000
Xtxp286	stg3	13		AGCAGCAGCAGCAACAG	GCGTGGTCTTTGTGGTTC	Bhattramakki et al. 2000
Stgnhsbm36	stg3	14		CTTTCGCCTGGTCGTACACT	AGAAGAACGCCTCGCTCTC	Srinivas et al. 2009
Xcup33	stgA	1	13.5577	GCGCTGCTGTGTGTTGTTC	ACGGGGATTAGCCTTTTAGG	Schloss et al. 2002
Xcup24	stgA	2	13.9567	AAACTGGATGCCACACCAAG	AGCTATACCAACACGGGCAG	Schloss et al. 2002
Xtxp357	sgtA	3	23.8062	CGCAGAAATACGATTG	GCTATCTGGAGTAACTGTGT	Bhattramakki et al. 2000
Xtxp329	stgA	4	50.1325	ACTACGAAGGTGTTTAGTTTAAGGG	CATTCATAAAACTAAACGAAAAACG	Bhattramakki et al. 2000
Xtxp043	stgA	5	50.2677	AGTCACAGCACACTGCTTGTC	AATTTACCTGGCGCTCTGC	Kong et al. 2000
Xtxp088	stgA	6	50.7095	CGTGAATCAGCGAGTGTTGG	TGCGTAATGTTCCTGCTC	Bhattramakki et al. 2000
Xtxp149	stgA	7	50.7111	AGCCTTGCATGATGTTCC	GCTATGCTTGGTGTGGG	Bhattramakki et al. 2000
Xtxp037	stgA	8	55.1238	AACCTAAGAGGCCTATTTAACC	ACGGCGACTCTGTAACTCATAG	Kong et al. 2000
Xtxp032	stgA	9		AGAAATTCACCATGCTGCAG	ACCTCACAGGCCATGTCG	Kong et al. 2000

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Conclusions

- Complex trait
- Breeding materials diversification
- Screening methodology
- Pedigree method works
- GGE significant
- MABS expedites QTL introgression

Relevant CGIAR Research Program

This work has been undertaken as part of the

CGIAR

RESEARCH PROGRAM ON
DrylandCereals

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Thank you

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